ЄXHIBIT6

Blast 2 Sequences results

| PubMed | Entrez | BLAST | OMIM | Taxonomy | Structure |

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2

x_dropoff: 50   expect: 10.000   wordsize: 11   Filter ☑   Align

| Sequence 1 | gi 4885194 | Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 3 (EDG3), mRNA | Length 1137 | (1 .. 1137) |
| Sequence 2 | lcl|seq_2 | | Length 23 | (1 .. 23) |
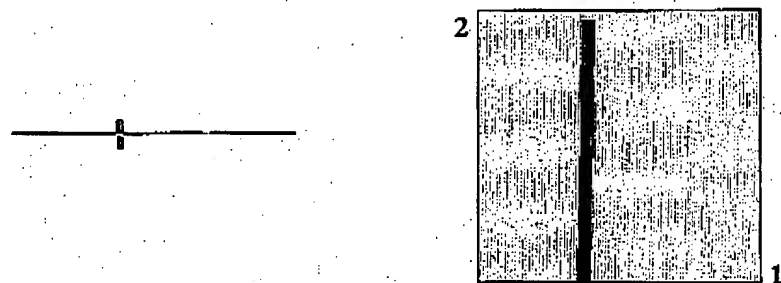
NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score = 44.9 bits (23), Expect = 0.17
Identities = 23/23 (100%)
 Strand = Plus / Plus
```

```
Query: 423  caaaatgaggccttacgacgcca 445
            |||||||||||||||||||||||
Sbjct: 1    caaaatgaggccttacgacgcca 23
```

```
CPU time:     0.05 user secs.      0.13 sys. secs      0.18 total secs.

Lambda      K       H
    1.33    0.621    1.12

Gapped
Lambda      K       H
    1.33    0.621    1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 1
```

Number of Sequences: 0
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
length of query: 1137
length of database: 5,006,917,935
effective HSP length: 24
effective length of query: 1113
effective length of database: 4,991,889,975
effective search space: 5555973542175
effective search space used: 5555973542175
T: 0
A: 30
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 20 (39.1 bits)